

#8

ENTERED<sup>OIPE</sup>

## RAW SEQUENCE LISTING

DATE: 03/13/2002

PATENT APPLICATION: US/09/897,427A

TIME: 11:52:31

Input Set : A:\78282558.app

Output Set: N:\CRF3\03132002\I897427A.raw

3 <110> APPLICANT: ADLER, JON ELLIOT  
4 LI, XIADONG  
5 STAZEWSKI, LENA  
6 XU, HONG  
7 EHEVERRI, FERNANDO  
9 <120> TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS  
11 <130> FILE REFERENCE: 078003-0282558  
13 <140> CURRENT APPLICATION NUMBER: 09/897,427A  
14 <141> CURRENT FILING DATE: 2001-07-03  
16 <160> NUMBER OF SEQ ID NOS: 10  
18 <170> SOFTWARE: PatentIn Ver. 2.1  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 2526  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Homo sapiens  
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53 aaagaagagt gggcacctga ggggaagccag acctgcttcc cgcgcactgt ggtgtttttg 1680
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57 ggctttcttg gggaaacctc aaggcctgcg tgcctgctac gccaggccct ctttgccctt 1920
58 ggtttcacca tcttctgtc ctgcctgaca gttcgctcat tccaactaat catcatcttc 1980
59 aagttttcca ccaaggtacc tacattctac cagcctggg tccaaaacca cgggtgctggc 2040
60 ctgtttgatg tgatcagctc agcggcccag ctgcttatct gtctaacttg gctggtggtg 2100
61 tggacccac tgctgctag ggaataccag cgcttcccc atctggtgat gcttgagtgc 2160
62 acagagacca actccctggg ctccatactg gccttccctt acaatggcct cctctccatc 2220
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68 acctga 2526

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71 &lt;210&gt; SEQ ID NO: 2

72 &lt;211&gt; LENGTH: 841

73 &lt;212&gt; TYPE: PRT

74 &lt;213&gt; ORGANISM: Homo sapiens

76 &lt;400&gt; SEQUENCE: 2

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81             20             25             30
83 Thr Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
84             35             40             45
86 Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
87             50             55             60
89 Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg
90   65             70             75             80
92 Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile
93             85             90             95
95 Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val
96             100            105            110
98 Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu
99             115            120            125
101 Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile
102             130            135            140
104 Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser
105   145            150            155            160
107 Pro Phe Leu Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu
108             165            170            175
110 Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp
111             180            185            190
113 Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp
114             195            200            205
116 Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly
117             210            215            220

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119 Val Gln Ala Leu Glu Asn Gln Ala Thr Gly Gln Gly Ile Cys Ile Ala
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122 Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met
123                245                250                255
125 Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val
126                260                265                270
128 Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val
129                275                280                285
131 Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala
132                290                295                300
134 Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met
135 305                310                315                320
137 Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala
138                325                330                335
140 Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Lys Ala Pro Arg Pro Cys
141                340                345                350
143 His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln
144                355                360                365
146 Ala Phe Met Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser
147                370                375                380
149 Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu
150 385                390                395                400
152 His Gln Leu Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val
153                405                410                415
155 Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu
156                420                425                430
158 His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser
159                435                440                445
161 Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr
162                450                455                460
164 Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu
165 465                470                475                480
167 Thr Lys Ile Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val
168                485                490                495
170 Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe
171                500                505                510
173 His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu
174                515                520                525
176 Asn Lys Ser Asp Leu Tyr Arg Cys Gln Pro Cys Gly Lys Glu Glu Trp
177                530                535                540
179 Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu
180 545                550                555                560
182 Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu
183                565                570                575
185 Leu Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu
186                580                585                590
188 Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met
189                595                600                605
191 Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly

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194 Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu
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197 Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu
198      645      650      655
200 Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala
201      660      665      670
203 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala
204      675      680      685
206 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu
207      690      695      700
209 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys
210 705      710      715      720
212 Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly
213      725      730      735
215 Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu
216      740      745      750
218 Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe
219      755      760      765
221 Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp
222      770      775      780
224 Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu
225 785      790      795      800
227 Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu
228      805      810      815
230 Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln
231      820      825      830
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234      835      840

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237 &lt;210&gt; SEQ ID NO: 3

238 &lt;211&gt; LENGTH: 2520

239 &lt;212&gt; TYPE: DNA

240 &lt;213&gt; ORGANISM: Homo sapiens

242 &lt;400&gt; SEQUENCE: 3

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245 ctccatgcca acatgaaggc cattgttcac cttaacttcc tgcaggtgcc catgtgcaag 180
246 gagtatgaag tgaaggatgat aggcataaac ctcatgcagg ccatgcgctt cgcggtggag 240
247 gagatcaaca atgacagcag cctgctgcct ggtgtgctgc tgggctatga gatcgtggat 300
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254 cagctgcttg gcgagcgcgt ggcccggcgc gacatctgca tcgccttcca ggagacgctg 720
255 cccacactgc agcccaacca gaacatgacg tcagaggagc gccagcgcct ggtgaccatt 780
256 gtggacaagc tgcagcagag cacagcgcgc gtgcgtggtc tgttctcgcc cgacctgacc 840
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260 tggggcccac aggtctgggcc gccacccctc agcaggacca gccagagcta tacctgcaac 1080
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262 ggggagcgtg tcgtctacag cgtgtactct gcggtctatg ctgtggccca tgccctgcac 1200
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265 caaggggacg tggctctgca cttggagatt gtccagtggc aatgggaccg gagccagaat 1380
266 cccttccaga gcgtcgcctc ctactacccc ctgcagcgac agctgaagaa catccaagac 1440
267 atctcctggc acaccgtcaa caacacgac cctatgtcca tgtgttccaa gaggtgccag 1500
268 tcagggcaaaa agaagaagcc tgtgggcatc cacgtctgct gcttcgagtg catcgactgc 1560
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287 &lt;210&gt; SEQ ID NO: 4

288 &lt;211&gt; LENGTH: 839

289 &lt;212&gt; TYPE: PRT

290 &lt;213&gt; ORGANISM: Homo sapiens

292 &lt;400&gt; SEQUENCE: 4

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297           20           25           30
299 Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
300       35           40           45
302 Val His Leu Asn Phe Leu Gln Val Pro Met Cys Lys Glu Tyr Glu Val
303       50           55           60
305 Lys Val Ile Gly Tyr Asn Leu Met Gln Ala Met Arg Phe Ala Val Glu
306       65           70           75           80
308 Glu Ile Asn Asn Asp Ser Ser Leu Leu Pro Gly Val Leu Leu Gly Tyr
309           85           90           95
311 Glu Ile Val Asp Val Cys Tyr Ile Ser Asn Asn Val Gln Pro Val Leu
312       100          105          110
314 Tyr Phe Leu Ala His Glu Asp Asn Leu Leu Pro Ile Gln Glu Asp Tyr
315       115          120          125
317 Ser Asn Tyr Ile Ser Arg Val Val Ala Val Ile Gly Pro Asp Asn Ser

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.



**VERIFICATION SUMMARY**

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L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9